

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/474,833DATE: 03/19/96
TIME: 17:02:06

INPUT SET: S10663.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Amgen Inc.

(ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 Dehavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 91230-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/474,833
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pessin, Karol M.
(C) REFERENCE/DOCKET NUMBER: A-345

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

51

52 TCTAGATTTG AGTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT 60

53

54 TCAGGACGAC ACCAAAACCT TAATTAAAC GATCGTTACG CGTATCAACG ACATCAGTCA 120

55

56 CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA 180

57

58 CCCGATCCTA AGCTTGTTCCA AAATGGACCA GACCCGTGGCT GTATACCAGC AGGTGTTAAC 240

59

60 CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT 300

61

62 GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA 360

63

64 ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT 420

65

66 GTCCCGTCTG CAGGGTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG 480

67

68 TTAATGGATC C 491

69

70 (2) INFORMATION FOR SEQ ID NO:2:

71

72 (i) SEQUENCE CHARACTERISTICS:

73 (A) LENGTH: 491 base pairs

74 (B) TYPE: nucleic acid

75 (C) STRANDEDNESS: double

76 (D) TOPOLOGY: linear

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78 (ii) MOLECULE TYPE: cDNA

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83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

84

85 AGATCTAAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA 60

86

87 AGTCCTGCTG TGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TGTAAGTCAGT 120

88

89 GTGGGTCAGC CAGAGGCGAT TTGTCGCACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT 180

90

91 GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG 240

92

93 GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA 300

94

95 CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT 360

96

97 TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAACGAGA 420

98

99 CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAA GAGGCCTTAC 480

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100
101 AATTACCTAG G 491
102
103 (2) INFORMATION FOR SEQ ID NO:3:
104
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 147 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS: single
109 (D) TOPOLOGY: linear
110
111 (ii) MOLECULE TYPE: protein
112
113
114
115
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
117
118 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
119 1 5 10 15
120
121 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
122 20 25 30
123
124 Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
125 35 40 45
126
127 Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
128 50 55 60
129
130 Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
131 65 70 75 80
132
133 Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
134 85 90 95
135
136 Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
137 100 105 110
138
139 Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
140 115 120 125
141
142 Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
143 130 135 140
144
145 Pro Glu Cys
146 145
147
148 (2) INFORMATION FOR SEQ ID NO:4:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 454 base pairs
152 (B) TYPE: nucleic acid

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153 (C) STRANDEDNESS: double
154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: cDNA
157
158
159
160
161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
162
163 CATATGGTAC CGATCCAGAA AGTTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT 60
164
165 ACGCGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTACAGGC 120
166
167 CTGGACTTCA TCCCGGGTCT GCACCCGATC CTGACCTTGT CCAAATGGA CCAGACCCTG 180
168
169 GCTGTATACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACGTTCCTCA GATCTCTAAC 240
170
171 GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG 300
172
173 CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGCG GGTTCCTGGA AGCATCCGGT 360
174
175 TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG 420
176
177 CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC 454
178
179 (2) INFORMATION FOR SEQ ID NO:5:
180
181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 454 base pairs
183 (B) TYPE: nucleic acid
184 (C) STRANDEDNESS: double
185 (D) TOPOLOGY: linear
186
187 (ii) MOLECULE TYPE: cDNA
188
189
190
191
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
193
194 GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA 60
195
196 TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTTGTTCG ACAATGTCCG 120
197
198 GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC 180
199
200 CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG 240
201
202 CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC 300
203
204 GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA 360
205

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206 ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAGTCCT GTACGAAACC 420
207
208 GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG 454
209

210 (2) INFORMATION FOR SEQ ID NO:6:
211

212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 147 amino acids
214 (B) TYPE: amino acid
215 (C) STRANDEDNESS: single
216 (D) TOPOLOGY: linear
217

218 (ii) MOLECULE TYPE: protein
219
220
221222
223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
224

225 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
226 1 5 10 15

227
228 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
229 20 25 30
230

231 Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
232 35 40 45
233

234 Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
235 50 55 60
236

237 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
238 65 70 75 80
239

240 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
241 85 90 95
242

243 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
244 100 105 110
245

246 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
247 115 120 125
248

249 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
250 130 135 140
251

252 Pro Gly Cys
253 145
254

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SEQUENCE VERIFICATION REPORT
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